

1 TATCCGCACCTCCGCTCCACCCGGCGCTCGGCGCGCCCGCCCTCCGATGCGCTCAGCG
 1 F-1006 M R S A
 61 GCCGCAGCTCCTCGGAGTCCCGCGGTGGCCACCGAGTCTCGCCGCTTCGCCGCAGCCAGG
 5 A A A P R S P A V A T E S R R F A A A R
 121 TGGCCCCGGGTGGCGCTCGCTCCAGCGGCCGGCGGGAGCGGGCGGGGCGGCGGTGGC
 25 W P G W R S L Q R P A R R S G R G G G G
 181 GCGGCCCCGGGACCGTATCCCTCCGCCGCCCTCCCCCGCCCGGCCCGGCCCTCC
 45 A A P G P Y P S A A P P P P G P G P P P
 241 TCCCGGCAGAGCTCGCCTCCCTCCGCTCAGACTGTTTTGGTAGCAACGGCAACGGCGGC
 65 S R Q S S P P S A S D C F G S N G N G G
 301 GGCGCGTTTCGGCCCCGGCTCCCGCGGCTCCTTGGTCTCGGCGGGCCTCCCCGCCCTTC
 85 G A F R P G S R R L L G L G G P P R P F R-1002
 361 GTCGTCGTCCTTCTCCCCCTCGCCAGCCCGGGCGCCCTCCGGCCGCGCCAACCCGCGCC
 105 V V V L L P L A S P G A P P A A P T R A
 421 TCCCGCTCGGCGCCCGTGCCTCCCGCCGCTTCCGGCGTCTCCTTGGCGCGCCCGGCT
 125 S P L G A R A S P P R S G V S L A R P A
 481 CCCGCTGTCCCCGCCCGGCTGCGAGCCGGTGTATGGGCCCCCTCACCATGTCGCTGAAG
 145 P G C P R P A C E P V Y G F-1 P L T M S L K
 541 CCCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAACAGCAGCAGCAGCAG
 165 P Q
 601 CAGCAGCAGCAGCCGCCCGCCCGGCTGCCAATGTCCGCAAGCCCGGCGGCAGCGGCCTT
 185 Q Q Q Q P P P A A A N V R K P R-2 G G S G L
 661 CTAGCGTCGCCCCGCCCGCGCCTTCGCCGTCCTCGTCTCCTCGTCTCCTCGGCC
 205 L A S R-1 P A A A P S P S S S S V S S S S A
 721 ACGGCTCCCTCCTCGGTGGTCCGCGGACCTCCGGCGGCGGGAGGCCCGGCCTGGGCAGA
 225 T A P S S V V A A T S G G G R P G L G R
 781 GGTGAAACAGTAACAAAGGACTGCCTCAGTCTACGATTTCTTTTGATGGAATCTATGCA
 245 G R N S N K G L P Q S T I S F D G I Y A
 841 AATATGAGGATGGTTTCATATACTTACATCAGTTGTTGGCTCCAAATGTGAAGTACAAGT
 265 N M R M V H I L T S V V G S K C E V Q V
 901 AAAAATGGAGGTATATATGAAGGAGTTTTTAAACTTACAGTCCGAAGTGTGATTTGGTA
 285 K N G G I Y E G V F K T Y S P K C D L V
 961 CTTGATGCCGCACATGAGAAAAGTACAGAATCCAGTTCGGGGCCGAAACGTGAAGAAATA
 305 L D A A H E K S T E S S S G P K R E E I
 1021 ATGGAGAGTATTTTGTTCAAATGTTTCAGACTTTGTTGTGGTACAGTTTAAAGATATGGAC
 325 M E S I L F K C S D F V V V Q F K D M D
 1081 TCCAGTTATGCAAAAAGAGATGCTTTTACTGACTCTGCTATCAGTGCTAAAGTGAATGGC
 345 S S Y A K R D A F T D S A I S A K V N G
 1141 GAACACAAAGAGAAGGACCTGGAGCCCTGGGATGCAGGTGAACACAGCCAATGAGGAA
 365 E H K E K D L E P W D A G E L T A N E E
 1201 CTTGAGGCTTTGGAAAATGACGTATCTAATGGATGGGATCCCAATGATATGTTTCGATAT
 385 L E A L E N D V S N G W D P N D M F R Y
 1261 AATGAAGAAAATTATGGTGTAGTGTCTACGTATGATAGCAGTTTATCTTCGTATACAGTG
 405 N E E N Y G V V S T Y D S S L S S Y T V

Fig. 1

1321 CCCTTAGAAAGAGATAACTCAGAAGAATTTTAAACGGGAAGCAAGGGCAAACCAGTTA
425 P L E R D N S E E F L K R E A R A N Q L
1381 GCAGAAGAAATTGAGTCAAGTGCCAGTACAAAGCTCGAGTGGCCCTGGAAAACGATGAT
445 A E E I E S S A Q Y K A R V A L E N D D
1441 AGGAGTGAGGAAGAAAAATACACAGCAGTTTCAGAGAAATCCAGTGAACGTGAGGGGCAC
465 R S E E E K Y T A V Q R N S S E R E G H
1501 AGCATAAACACTAGGGAAAATAAATATATTCCTCCTGGACAAAGAAATAGAGAAGTCATA
485 S I N T R E N K Y I P P G Q R N R E V I
1561 TCCTGGGGAAGTGGGAGACAGAATTCACCGGTATGGGCCAGCCTGGATCGGGCTCCATG
505 S W G S G R Q N S P R M G Q P G S G S M
1621 CCATCAAGATCCACTTCTCACACTTCAGATTTCAACCCGAATTCTGGTTTCAGACCAAAGA
525 P S R S T S H T S D F N P N S G S D Q R
1681 GTAGTTAATGGAGGTGTTCCCTGGCCATCGCCTTGCCCATCTCCTCCTCTCGCCACCT
545 V V N G G V P W P S P C P S P S S R P P
1741 TCTCGCTACCAGTCAGGTCCCAACTCTCTCCACCTCGGGCAGCCACCCCTACACGGCCG
565 S R Y Q S G P N S L P P R A A T P T R P
1801 CCCTCCAGGCCCCCTCGCGCCATCCAGACCCCGTCTCACCCCTCTGCTCATGGTTCT
585 P S R P P S R P S R P P S H P S A H G S
1861 CCAGCTCCTGTCTCTACTATGCCTAAACGCATGTCTTCAGAAGGGCCTCCAAGGATGTCC
605 P A P V S T M P K R M S S E G P P R M S
1921 CCAAAGGCCCAGCGACATCCTCGAAATCACAGAGTTTCTGCTGGGAGGGGTTCCATATCC
625 P K A Q R H P R N H R V S A G R G S I S
1981 AGTGGCCTAGAATTTGTATCCCACAACCCACCCAGTGAAGCAGCTACTCCTCCAGTAGCA
645 S G L E F V S H N P P S E A A T P P V A
2041 AGGACCAGTCCCTCGGGGGGAACGTGGTCATCAGTGGTCAGTGGGGTTCCAAGATTATCC
665 R T S P S G G T W S S V V S G V P R L S
2101 CCTAAAACTCATAGACCCAGGTCTCCAGACAGAACAGTATTGGAAATACCCCCAGTGGG
685 P K T H R P R S P R Q N S I G N T P S G
2161 CCAGTTCTTGCTTCTCCCAAGCTGGTATTATTCCAAGTGAAGCTGTTGCCATGCCTATT
705 P V L A S P Q A G I I P T E A V A M P I
2221 CCAGCTGCATCTCCTACGCCTGCTAGTCCCTGCATCGAACAGAGCTGTTACCCCTTCTAGT
725 P A A S P T P A S P A S N R A V T P S S
2281 GAGGCTAAAGATTCCAGGCTTCAAGATCAGAGGCAGAACTCTCCTGCAGGGAATAAAGAA
745 E A K D S R L Q D Q R Q N S P A G N K E
2341 AATATTAAACCAATGAAACATCACCTAGCTTCTCAAAAGCTGAAAACAAAGGTATATCA
765 N I K P N E T S P S F S K A E N K G I S
2401 CCAGTTGTTTCTGAACATAGAAAACAGATTGATGATTTAAAGAAATTTAAGAATGATTTT
785 P V V S E H R K Q I D D L K K F K N D F
2461 AGGTTACAGCCAAGTTCTACTTCTGAATCTATGGATCAACTACTAAACAAAAATAGAGAG
805 R L Q P S S T S E S M D Q L L N K N R E
2521 GGAGAAAAATCAAGAGATTTGATCAAAGACAAAATTGAACCAAGTGCTAAGGATTCTTTC
825 G E K S R D L I K D K I E P S A K D S F
2581 ATTGAAAATAGCAGCAGCAACTGTACCAGTGGCAGCAGCAAGCCGAATAGCCCCAGCATT
845 I E N S S S N C T S G S S K P N S P S I

Fig. 2

2641 TCCCCTTCAATACTTAGTAACACGGAGCACAAGAGGGGACCTGAGGTCACTTCCCCAAGGG
865 S P S I L S N T E H K R G P E V T S Q G
2701 GTTCAGACTTCCAGCCCAGCATGTAAACAAGAGAAAGACGATAAGGAAGAGAAGAAAGAC
885 V Q T S S P A C K Q E K D D K E E K K D
2761 GCAGCTGAGCAAGTTAGGAAATCAACATTGAATCCCAATGCAAAGGAGTTCAACCCACGT
905 A A E Q V R K S T L N P N A K E F N P R
2821 TCCTTCTCTCAGCCAAAGCCTTCTACTACCCCAACTTCACCTCGGCCTCAAGCACAACT
F-13
925 S F S Q P K P S T T P T S P R P Q A Q P
2881 AGCCCATCTATGGTGGGTATCAACAGCCAACTCCAGTTTATACTCAGCCTGTTTGTTTT
945 S P S M V G H Q Q P T P V Y T Q P V C F
2941 GCACCAAATATGATGTATCCAGTCCCAGTGAGCCCAGGCGTGCAACCTTTATACCCAATA
965 A P N M M Y P V P V S P G V Q P L Y P I
3001 CCTATGACGCCCATGCCAGTGAATCAAGCCAAGACATATAGAGCAGTACCAAATATGCCC
985 P M T P M P V N Q A K T Y R A V P N M P
3061 CAACAGCGGCAAGACCAGCATCATCAGAGTGCCATGATGCACCCAGCGTCAGCAGCGGGC
1005 Q Q R Q D Q H H Q S A M M H P A S A A G
3121 CCACCGATTGCAGCCACCCACAGCTTACTCCACGCAATATGTTGCCTACAGTCCTCAG
1025 P P I A A T P P A Y S T Q Y V A Y S P Q
3181 CAGTTCCCAAATCAGCCCCCTTGTTTCAGCATGTGCCACATTATCAGTCTCAGCATCCTCAT
1045 Q F P N Q P L V Q H V P H Y Q S Q H P H
3241 GTCTATAGTCCTGTAATACAGGGTAATGCTAGAATGATGGCACCACCAACACACGCCCAG
1065 V Y S P V I Q G N A R M M A P P T H A Q
3301 CCTGGTTTATGATCTTCTTCAGCAACTCAGTACGGGGCTCATGAGCAGACGCATGCGATG
1085 P G L V S S S A T Q Y G A H E Q T H A M
3361 TATGCATGTCCCAAATTACCATAACAAGGAGACAAGCCCTTCTTTTACTTTGCCATT
1105 Y A C P K L P Y N K E T S P S F Y F A I
3421 TCCACGGGCTCCCTTGCTCAGCAGTATGCGCACCCCTAACGCTACCCTGCACCCACATACT
1125 S T G S L A Q Q Y A H P N A T L H P H T
3481 CCACACCCTCAGCCTTCAGCTACCCCCACTGGACAGCAGCAAAGCCAACATGGTGGAAGT
1145 P H P Q P S A T P T G Q Q Q S Q H G G S
3541 CATCCTGCACCCAGTCCTGTTTCAGCACCATCAGCACCAGGCCGCCAGGCTCTCCATCTG
1165 H P A P S P V Q H H Q H Q A A Q A L H L
3601 GCCAGTCCACAGCAGCAGTCAGCCATTTACCACGCGGGGCTTGCGCCAACTCCACCCTCC
1185 A S P Q Q Q S A I Y H A G L A P T P P S
3661 ATGACACCTGCCTCCAACACGCAGTCGCCACAGAATAGTTTCCCAGCAGCACAACAGACT
1205 M T P A S N T Q S P Q N S F P A A Q Q T
3721 GTCTTTACGATCCATCCTTCTCAGTTTCAGCCGGCGTATACCAACCCACCCACATGGCC
1225 V F T I H P S H V Q P A Y T N P P H M A
3781 CACGTACCTCAGGCTCATGTACAGTCAGGAATGGTTCTTCTCATCCAAGTGGCCATGCG
1245 H V P Q A H V Q S G M V P S H P T A H A
3841 CCAATGATGCTAATGACGACACAGCCACCCGCGGTCCCCAGGCCGCCCTCGCTCAAAGT
1265 P M M L M T T Q P P G G P Q A A L A Q S
3901 GCACTACAGCCCATTCCAGTCTCGACAACAGCGCATTTCCCTTATATGACGCACCCCTTCA
1285 A L Q P I P V S T T A H F P Y M T H P S
3961 GTACAAGCCCACCACCAACAGCAGTTGTAAGGCTGCCCTGGAGGAACCGAAAGGCCAAAT
1305 V Q A H H Q Q Q L *

Fig. 3

4021 TCCCTCCTCCCTTCTACTGCTTCTACCAACTGGAAGCACAGAAAAGCTAGAATTTTCATTTA
 4081 TTTTGT TTTTAAAATATATATGTTGATTTCTTGTAACATCCAATAGGAATGCTAACAGTT
 4141 CACTTGCAAGTGAAGATACTTGGACCGAGTAGAGGCATTTAGGAAGTTGGGGGCTATTCC
 4201 ATAATTCCATATGCTGTTTCAGAGTCCCGCAGGTACCCAGCTCTGCTTGCCGAAACTGG
 4261 AAGTTATTTATTTTAAATAACCCTTGAAAGTCATGAACACATCAGCTAGCAAAAAGAAGT
 4321 AACAAGAGTGATTCTTGCTGCTATTACTGCT (A)_n

Fig. 4

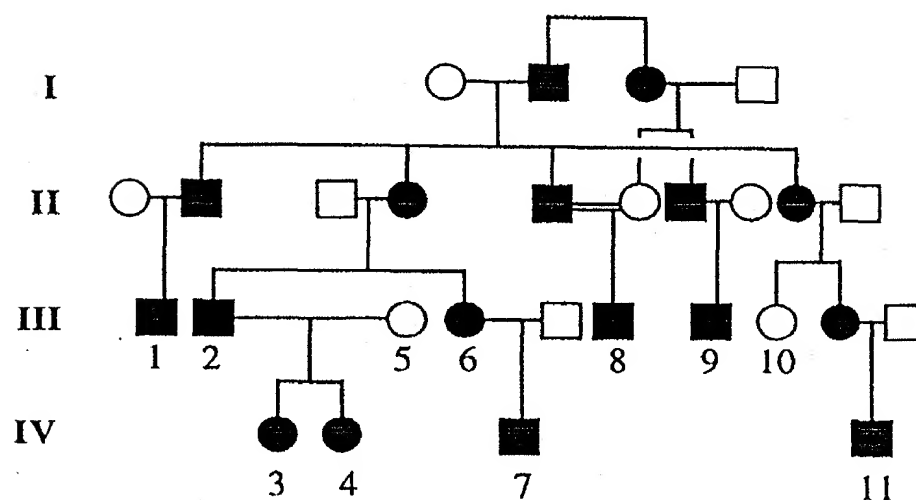


Fig. 5

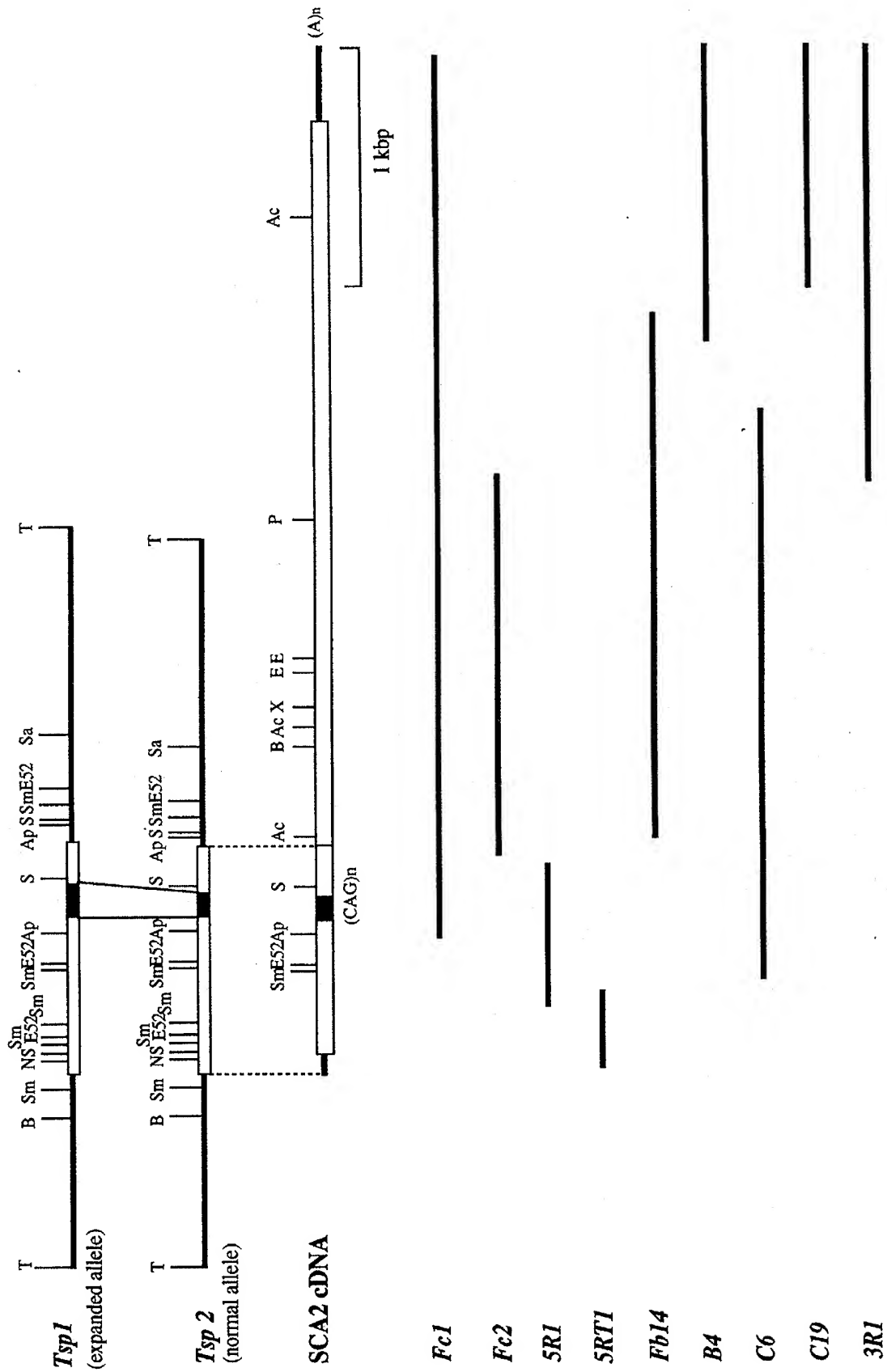


Fig. 6

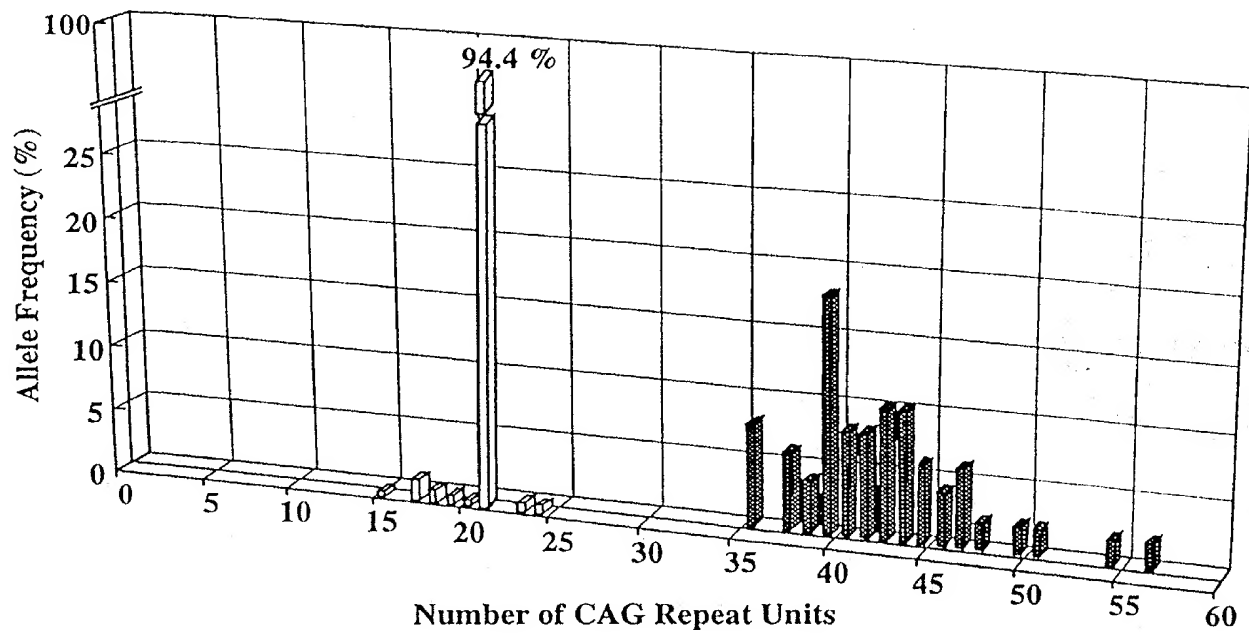


Fig. 7